



SEQUENCE LISTING

*a8*  
<110> Duvick, Johnathan P.

Gilliam, Jacob T.

Maddox, Joyce R.

Rao, Aragula Gururaj

Crasta, Oswald R.

Folkerts, Otto

<120> Amino Polyol Aamine Oxidase Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<140> US 09/658,835

<141> 2000-09-08

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<151> 1999-07-12

<150> US 09/352,168

<151> 1999-07-12

<160> 54

<170> PatentIn version 3.1

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<213> Exophiala spinifera

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<221> misc\_feature

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt 180  
ggaggacgcc cgagaagcct tggcgcc accacggctt gtcccatacg aagactatct 240  
tgctata tagta gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg 300  
gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc ttttgcttc 360  
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tacaaggttg tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccgaggcc 120  
gatcgtaactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180  
ac 182

<210> 3  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 3  
tggtttcgtt accgacaacc ttgttatccc 29

<210> 4  
<211> 28  
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gagttggtcc cagacagact tttgtcgt 28

<210> 5  
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96  
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336  
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480  
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt 528  
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag 576  
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg 624  
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly Gly

195	200	205	
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210	215	220	672
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225	230	235	720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245	250	255	768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu 260	265	270	816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275	280	285	864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290	295	300	912
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln 305	310	315	960
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val 325	330	335	1008
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga ccg Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg 340	345	350	1056
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp 355	360	365	1104
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro 370	375	380	1152
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly 385	390	395	1200
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg Ala Pro Ser Ala Val Tyr Glu Leu Asn Asp Leu Ile Thr Leu Gly Ser 405	410	415	1248
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr 420	425	430	1296

tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa 1344  
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
435 440 445

cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1389  
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 6

<211> 462

<212> PRT

<213> Exophiala spinifera

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20 25 30

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35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
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<210> 7

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<213> Exophiala spinifera

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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336  
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480  
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt 528  
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

gtg gaa gcc cac gag atc agc atg ctt ctc acc gac tac atc aag 576  
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg 624

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
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Gln Tyr Val Arg Cys Lys Thr			
210	215		
ctcgtttctc agtggtcatt cca ggt atg cag tcg att tgc cat gcc atg tca			728
Gly Met Gln Ser Ile Cys His Ala Met Ser			
220	225		
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa			776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu			
230	235	240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc			824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala			
245	250	255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat			872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr			
260	265	270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg			920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu			
275	280	285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg			968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			
290	295	300	305
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg			1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			
310	315	320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat			1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
325	330	335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag			1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
340	345	350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
355	360	365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
370	375	380	385
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
390	395	400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Thr Leu Gly Ser Ala			

405	410	415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg acg tct Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			1352
420	425	430	
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435	440	445	
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly 35 40 45			
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp 50 55 60			
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu 65 70 75 80			
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp 85 90 95			
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu 100 105 110			
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile 115 120 125			

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
245 250 255

Ala Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu  
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
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<212> PRT

<213> Exophiala spinifera

<400> 9

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20 25 30

Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly  
210 215 220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met  
225 230 235 240

Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro  
245 250 255

Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro  
260 265 270

Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln  
275 280 285

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys

290	295	300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr		
305	310	315
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn		
325	330	335
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser		
340	345	350
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly		
355	360	365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr		
370	375	380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg		
385	390	395
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu		
405	410	415
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg		
420	425	430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu		
435	440	445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr		
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<222> (1)..(1389)

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 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly  
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 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30  
  
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45  
  
 ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60  
  
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80  
  
 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95  
  
 gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag  
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110  
  
 gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125  
  
 atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 130 135 140  
  
 cggtt gca agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac  
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175	528
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205	624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210 215 220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255	768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	
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<211> 463			
<212> PRT			
<213> Exophiala spinifera			
<220>			
<221> misc_feature			
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<223> Extra lysine in K:trAPAO			
<400> 11			
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly			
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Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			
20	25	30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
35	40	45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			

65	70	75	80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors,  
N23256

<400> 12  
gggaaattca aagacaacgt tgccggacgtg gtag 34

<210> 13  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer sequence designed for cloning DNA into expression vectors N23256

<400> 13  
ggggcggccg cctatgctgc tggcaccagg ctag 34

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide for 3' RACE, N21965  
<400> 14  
tggtttcgtt accgacaacc ttgttatccc 29

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide for 5' RACE, N21968  
<400> 15  
gagttggtcc cagacagact tttgtcgt 28

<210> 16  
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<212> DNA  
<213> Exophiala spinifera

<220>  
<221> sig\_peptide  
<222> (1)..(267)  
<223> yeast alpha mating factor secretion signal

<220>  
<221> CDS  
<222> (1)..(1662)  
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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
1 5 10 15  
  
gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96  
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln  
20 25 30  
  
att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144  
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
35 40 45  
  
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192  
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
50 55 60  
  
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240  
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
65 70 75 80  
  
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg 288  
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala  
85 90 95

gac gtg gta gtg gtc ggc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 100 105 110	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 115 120 125	384
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 130 135 140	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 145 150 155 160	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 165 170 175	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 180 185 190	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 195 200 205	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 210 215 220	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 225 230 235 240	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 245 250 255	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 260 265 270	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 275 280 285	864
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg 290 295 300	912
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 305 310 315 320	960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			
325	330	335	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtc ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
340	345	350	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
355	360	365	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
370	375	380	
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
385	390	395	400
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
405	410	415	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
420	425	430	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
435	440	445	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
450	455	460	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
465	470	475	480
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
485	490	495	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
500	505	510	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
515	520	525	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca			1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala			
530	535	540	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c			1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala			

545

550

<210> 17

<211> 554

<212> PRT

<213> *Exophiala spinifera*

<400> 17

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
65 70 75 80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala  
85 90 95

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg  
100 105 110

Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp  
115 120 125

Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr  
130 135 140

Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser  
145 150 155 160

Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln  
165 170 175

Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr  
180 185 190

Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala  
195 200 205

Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser  
210 215 220

Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val  
225 230 235 240

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu  
245 250 255

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His  
260 265 270

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly  
275 280 285

Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg  
290 295 300

Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu  
305 310 315 320

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln  
325 330 335

Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg  
340 345 350

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu  
355 360 365

Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn  
370 375 380

Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro  
385 390 395 400

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp  
405 410 415

Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp  
420 425 430

Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln  
435 440 445

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala  
450 455 460

Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu  
465 470 475 480

Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala  
485 490 495

Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr  
500 505 510

Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp  
515 520 525

Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala  
530 535 540

Glu Val Val Ala Ser Leu Val Pro Ala Ala  
545 550

<210> 18

<211> 2079

<212> DNA

<213> Unknown

<220>

<223> GST:K:trAPAO 2079 for bacterial expression

<220>

<221> CDS

<222> (1)..(2076)

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<222> (1)..(687)

<223> gst fusion + polylinker

<220>

<221> misc\_feature

<222> (688)..(2076)

<223> K:trAPAO

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<221> misc\_feature

<222> (688)..(690)

<223> Extra lysine

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1 5 10 15

48

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg  
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30

96

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

144

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

192

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn

240

65	70	75	80	
atg ttg ggt ggt tgc cca aaa gag cgt gca gag att tca atg ctt gaa Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95				288
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110				336
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125				384
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140				432
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160				480
gtt gtt tta tac atg gac cca atg tgc gat gcg ttc cca aaa tta Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175				528
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190				576
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205				624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220				672
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly 225 230 235 240				720
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 245 250 255				768
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 260 265 270				816
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285				864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300				912

gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305                   310                   315                   320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 325                   330                   335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340                   345                   350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355                   360                   365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370                   375                   380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385                   390                   395                   400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405                   410                   415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser 420                   425                   430	1296
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435                   440                   445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450                   455                   460	1392
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465                   470                   475                   480	1440
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485                   490                   495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500                   505                   510	1536
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr 515                   520                   525	1584

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly 530 535 540	1632
ttc tcg ggc gtc ctccaa tcg agc tgt gac ccc atc tca ttt gcc aga Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg 545 550 555 560	1680
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met 565 570 575	1728
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg 580 585 590	1776
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly 595 600 605	1824
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys 610 615 620	1872
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp 625 630 635 640	1920
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His 645 650 655	1968
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly 660 665 670	2016
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu 675 680 685	2064
gtg cca gca gca tag Val Pro Ala Ala 690	2079

<210> 19

<211> 692

<212> PRT

<213> Unknown

<220>

```

<223> GST:K:trAPAO 2079  for bacterial expression

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst fusion + polylinker

<220>

<221> misc_feature

<222> (688)..(2076)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (688)..(690)

<223> Extra lysine

<400> 19

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1                      5                  10                  15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20                     25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35                     40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50                     55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                     70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85                     90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100                    105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

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115	120	125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		
130	135	140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp		
145	150	160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu		
165	170	175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr		
180	185	190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala		
195	200	205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg		
210	215	220
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly		
225	230	235
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly		
245	250	255
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr		
260	265	270
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly		
275	280	285
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe		
290	295	300
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser		
305	310	315
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp		
325	330	335
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro		
340	345	350

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
355 360 365

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
370 375 380

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
385 390 395 400

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
405 410 415

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
420 425 430

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
435 440 445

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
450 455 460

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
465 470 475 480

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
485 490 495

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
530 535 540

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
545 550 555 560

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
565 570 575

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
580 585 590

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
595 600 605

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
610 615 620

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
625 630 635 640

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
645 650 655

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
660 665 670

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
675 680 685

Val Pro Ala Ala  
690

<210> 20

<211> 1464

<212> DNA

<213> Unknown

<220>

<223> K:trAPAO translational fusion with barley alpha amylase

<220>

<221> sig\_peptide

<222> (1)..(72)

<223> Barley alpha amylase signal sequence

<220>  
 <221> misc\_feature  
 <222> (73)..(1464)  
 <223> K:trAPAO cDNA

<220>  
 <221> CDS  
 <222> (1)..(1461)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (73)..(75)  
 <223> Added lysine residue

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly		
1 5 10 15		
ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta		96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val		
20 25 30		
gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag		144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln		
35 40 45		
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg		192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly		
50 55 60		
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac		240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn		
65 70 75 80		
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc		288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser		
85 90 95		
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act		336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr		

100	105	110	
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro			384
115 120 125			
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu			432
130 135 140			
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp			480
145 150 155 160			
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala			528
165 170 175			
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala			576
180 185 190			
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser			624
195 200 205			
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn			672
210 215 220			
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr			720
225 230 235 240			
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly			768
245 250 255			
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser			816
260 265 270			
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys			864
275 280 285			
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser			912
290 295 300			
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu			960
305 310 315 320			
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg			1008
325 330 335			

gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca		1056	
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser			
340	345	350	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc		1104	
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr			
355	360	365	
tgt ttc atg gtc gga gac ccg gga cg <sup>g</sup> aag tgg tcc caa cag tcc aag		1152	
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
370	375	380	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag		1200	
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			
385	390	395	400
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag		1248	
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			
405	410	415	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg		1296	
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
420	425	430	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag		1344	
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
435	440	445	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat		1392	
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
450	455	460	
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg		1440	
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
465	470	475	480
gct agc ctg gtg cca gca gca tag		1464	
Ala Ser Leu Val Pro Ala Ala			
485			

<210> 21

<211> 487

<212> PRT

<213> Unknown

<220>

<223> K:trAPAO translational fusion with barley alpha amylase

<220>

<221> misc\_feature  
<222> (73)..(1464)  
<223> K:trAPAO cDNA  
  
<220>  
  
<221> misc\_feature  
<222> (73)..(75)  
<223> Added lysine residue  
  
<400> 21

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
1 5 10 15

Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
20 25 30

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
35 40 45

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
50 55 60

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
65 70 75 80

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
85 90 95

Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
100 105 110

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
115 120 125

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
130 135 140

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
145 150 155 160

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
165 170 175

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
180 185 190

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
195 200 205

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
210 215 220

Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
225 230 235 240

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
245 250 255

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
260 265 270

Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys  
275 280 285

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser  
290 295 300

Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu  
305 310 315 320

Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg  
325 330 335

Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser  
340 345 350

Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr  
355 360 365

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys  
370 375 380

Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu

385

390

395

400

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu  
405 410 415

Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly  
420 425 430

Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys  
435 440 445

Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr  
450 455 460

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val  
465 470 475 480

Ala Ser Leu Val Pro Ala Ala  
485

<210> 22

<211> 1803

<212> DNA

<213> Exophiala spinifera

<220>

<221> CDS

<222> (1)..(1800)

<223>

<400> 22

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1 5 10 15  
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96  
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96  
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct 144

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro			
35	40	45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys			
50	55	60	192
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr			
65	70	75	80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly			
85	90	95	288
ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val			
100	105	110	336
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala			
115	120	125	384
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val			
130	135	140	432
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc gta gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc			
145	150	155	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
160			480
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
165	170	175	528
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
180	185	190	576
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val			
195	200	205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr			
210	215	220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala			
225	230	235	720
240			
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
245	250	255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
			816

260	265	270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
275	280	285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta			912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
290	295	300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc			960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
305	310	315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt			1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
325	330	335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa			1056
Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
340	345	350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca			1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
355	360	365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca			1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
370	375	380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
385	390	395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			1248
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
405	410	415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
420	425	430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
435	440	445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
450	455	460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475	480
acc tgt ttc atg gtc gga gac ccg gga cg aag tgg tcc caa cag tcc			1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
485	490	495	

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	500	505	510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	515	520	525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	530	535	540	1632
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	545	550	555	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	565	570	575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	580	585	590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala	595	600		1803
<210> 23				
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<212> PRT				
<213> Exophiala spinifera				
<400> 23				
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro 1 5 10 15				
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val 20 25 30				
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35 40 45				
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50 55 60				

Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65				70				75					80		
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90					95		
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105				110			
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
			115				120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
			130			135				140					
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
			145			150			155			160			
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165				170				175				
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180				185				190				
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
			195			200			205						
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
			210			215			220						
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
			225			230			235			240			
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			245				250				255				
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
			260				265			270					
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
			275				280				285				

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile

515

520

525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
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1                   5                   10                   15		
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct		96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala		
20                   25                   30		
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc		144
Gly Met Val Val Gly Thr Thr Val Pro Gly Thr Thr Ala Thr		
35                   40                   45		
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt		192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe		
50                   55                   60		
gcu cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act		240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr		
65                   70                   75                   80		
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc		288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu		
85                   90                   95		
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt		336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly		

100	105	110	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu			384Glu Ser
115	120	125	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu			432
130	135	140	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala			480
145	150	155	160
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu			528
165	170	175	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly			576
180	185	190	
ttc cta gaccaa agg ttt gct ttg gat tgg gta cag cgg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala			624
195	200	205	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala			672
210	215	220	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro			720
225	230	235	240
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe			768Pro Phe
245	250	255	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Val Gln Ala Leu			816
260	265	270	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp			864
275	280	285	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu			912
290	295	300	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg			960
305	310	315	320
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala			1008
325	330	335	

aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat		1056	
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr			
340	345	350	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt		1104	
Leu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
355	360	365	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag		1152Gly Ala	
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
370	375	380	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc		1200	
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
385	390	395	400
gtg gct cag gac tcc cg <sup>g</sup> aat cg <sup>g</sup> ggt atc cct tct tgg cg <sup>c</sup> tac tac		1248	
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
405	410	415	
tac aat gc <sup>g</sup> acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg		1296	
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
420	425	430	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc ac <sup>g</sup> tat cct gtc gca		1344	
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
435	440	445	
agt gc <sup>g</sup> acc gc <sup>c</sup> ttg gag gc <sup>c</sup> cag ac <sup>g</sup> ac <sup>g</sup> aaa tac atg cag ggt gc <sup>c</sup>		1392	
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
450	455	460	
tgg gc <sup>c</sup> gcc ttt gc <sup>c</sup> aaa aac cc <sup>c</sup> atg aat ggg cct ggg tgg aaa caa		1440	
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
465	470	475	480
gtg cc <sup>g</sup> aat gtc gc <sup>g</sup> gc <sup>g</sup> ctt ggc tca cca ggc aaa gc <sup>c</sup> atc cag gtt		1488	
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
485	490	495	
gac gtc tct cca gc <sup>g</sup> aca ata gac caa cga tgt gc <sup>c</sup> ttg tac ac <sup>g</sup> cgt		1536Asp Val	
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
500	505	510	
tat tat act gag ttg ggc aca atc gc <sup>g</sup> cc <sup>g</sup> agg aca ttt ggc gga ggc		1584	
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
515	520	525	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gc <sup>g</sup> gac gtg		1632	
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
530	535	540	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag ac <sup>g</sup> gca cg <sup>c</sup> aaa gtc		1680	
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
545	550	555	560

cag gcc gcc ggt ctg tcc tgc ctc gtt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 565 570 575	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 580 585 590	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 595 600 605	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 610 615 620	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 625 630 635 640	1920Thr Gly
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 645 650 655	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 660 665 670	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 675 680 685	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 690 695 700	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 705 710 715 720	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 725 730 735	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 740 745 750	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 755 760 765	2304Thr Gly
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 770 775 780	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	2400

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
785	790	795	800
aag gtg gtc ttc tca ccc gag aac acc ttg tat ccc acc ttg aca ttt			2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
805	810	815	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
820	825	830	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
835	840	845	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
850	855	860	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
865	870	875	880
acc tgt ttc atg gtc gga gac ccg gga aag tgg tcc caa cag tcc			2688Thr Cys
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
885	890	895	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac			2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
900	905	910	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc			2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
915	920	925	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
930	935	940	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
945	950	955	960
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg			2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
965	970	975	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
980	985	990	
gtg gct agc ctg gtg cca gca gca tag			3003
Val Ala Ser Leu Val Pro Ala Ala			
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20          25          30

Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
35          40          45

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Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
50 55 60

Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr  
65 70 75 80

Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu  
85 90 95

Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly  
100 105 110

Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu  
115 120 125

Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu  
130 135 140

Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala  
145 150 155 160

Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu  
165 170 175

Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly  
180 185 190

Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala  
195 200 205

Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala  
210 215 220

Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro  
225 230 235 240

Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe  
245 250 255

Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu  
260 265 270

Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp  
275 280 285

Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu  
290 295 300

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg  
305 310 315 320

Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala  
325 330 335

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr  
340 345 350

Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu  
355 360 365

Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln  
370 375 380

Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile  
385 390 395 400

Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr  
405 410 415

Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val  
420 425 430

Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala  
435 440 445

Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala  
450 455 460

Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln  
465 470 475 480

Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val  
485 490 495

Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg  
500 505 510

Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly  
515 520 525

Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val  
530 535 540

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
545 550 555 560

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
565 570 575

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
580 585 590

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
595 600 605

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
610 615 620

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
625 630 635 640

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
645 650 655

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
660 665 670

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
675 680 685

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
690 695 700

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
705 710 715 720

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser

725

730

735

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
740 745 750

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
755 760 765

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
770 775 780

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
785 790 795 800

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
805 810 815

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
820 825 830

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
835 840 845

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
850 855 860

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
865 870 875 880

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
885 890 895

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
900 905 910

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
915 920 925

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
930 935 940

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
945 950 955 960

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
965 970 975

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
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Val Ala Ser Leu Val Pro Ala Ala  
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<223> Barley alpha amylase signal sequence

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly		
-20                  -15                  -10		
ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc		96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr		
-5                  -1    1                  5		
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc		144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg		
10                  15                  20		
gga ata ccc tat gca gcg ccg ctc gtc ggg ctg cgt tgg aag ccg		192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro		
25                  30                  35                  40		
ccc caa cac gcc ccg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt		240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe		
45                  50                  55		
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc		288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala		
60                  65                  70		

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	75	80	85	336
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	90	95	100	384
ggc ttc gcc ggc ggc acg gcc atg ccc tac tac gac ggc gag gcg Gly Phe Ala Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	105	110	115	432
ctt gcg cga cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	125	130	135	480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc Ile Leu Gly Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	140	145	150	528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Ala Ala Leu Arg	155	160	165	576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	170	175	180	624
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	185	190	195	672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	205	210	215	720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	220	225	230	768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	235	240	245	816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	250	255	260	864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	265	270	275	912
ccg cag acc gac agc gcg gcg atc gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Gly Gln Leu Ala Pro Val	285	290	295	960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg				1008

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly			
300	305	310	
 cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg			1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala			
315	320	325	
 cag ttt ggc gac caa gcc gcc gtc gtc gtc tat ccc ctc gac			1104
Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp			
330	335	340	
 ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat			1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn			
345	350	355	360
 cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag			1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln			
365	370	375	
 ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga			1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly			
380	385	390	
 aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg			1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val			
395	400	405	
 ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc			1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro			
410	415	420	
 acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc			1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val			
425	430	435	440
 cggttcgccaaatggc gaccccggggacgcccttacc tgg cct			1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro			
445	450	455	
 gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc			1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg			
460	465	470	
 gcgcgtgtgtccggaccccttccatccccccttgccgcgtatggc			1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly			
475	480	485	
 gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc			1584
Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser			
490	495	500	
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt			1632
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly			
505	510	515	520
 ttg gag acg gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt			1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			

525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 540	545	550	1728
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 555	560	565	1776
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 570	575	580	1824
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 585	590	595	1872
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 605	610	615	1920
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 620	625	630	1968
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 635	640	645	2016
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 650	655	660	2064
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 665	670	675	2112
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685	690	695	2160
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700	705	710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715	720	725	2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730	735	740	2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745	750	755	2352
			760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 765 770 775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795 800 805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810 815 820	2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840	2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 855	2640
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890 895 900	2784
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 905 910 915 920	2832
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 925 930 935	2880
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 940 945 950	2928
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 955 960 965	2976

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<212> PRT

<213> Unknown

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<222> (1546)..(1584)

<223> spacer sequence

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<222> (1585)..(1587)

<223> Extra lysine

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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr  
-5 -1 1 5

Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg  
10 15 20

Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro  
25 30 35 40

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe  
45 50 55

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala  
60 65 70

Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser  
75 80 85

Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly  
90 95 100

Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala  
105 110 115 120

Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn  
125 130 135

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
155 160 165

Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
170 175 180

Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
185 190 195 200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser  
205 210 215

Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser  
220 225 230

Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro  
235 240 245

Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp  
250 255 260

Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu  
265 270 275 280

Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val  
285 290 295

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly  
300 305 310

Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala  
315 320 325

Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp  
330 335 340

Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn  
345 350 355 360

Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln  
365 370 375

Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly  
380 385 390

Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val  
395 400 405

Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro  
410 415 420

Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val  
425 430 435 440

Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro  
445 450 455

Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg  
460 465 470

Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly  
475 480 485

Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser  
490 495 500

Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly

505                   510                   515                   520  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
525   530                                 535  
  
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
540   545                                 550  
  
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
555   560                                 565  
  
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
570   575                                 580  
  
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
585   590                                 595                             600  
  
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
605   610                                 615  
  
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
620   625                                 630  
  
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
635   640                                 645  
  
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
650   655                                 660  
  
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
665   670                                 675                             680  
  
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
685   690                                 695  
  
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
700   705                                 710  
  
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
715   720                                 725  
  
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
730   735                                 740

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
745 750 755 760

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
765 770 775

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
780 785 790

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
795 800 805

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
810 815 820

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
825 830 835 840

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
845 850 855

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
860 865 870

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
875 880 885

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
890 895 900

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
905 910 915 920

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
925 930 935

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
940 945 950

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
955 960 965

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<211> 3618

<212> DNA

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<222> (1)..(3615)

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<223> espl mat
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<223> spacer sequence
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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
          -225           -220           -215

ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag      90
Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
          -210           -205           -200

cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag      135
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
          -195           -190           -185

ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat      180
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
          -180           -175           -170

ggg gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata      225
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
          -165           -160           -155

gct gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca      270
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
          -150           -145           -140

gag att tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt      315
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
          -135           -130           -125

gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt      360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val
          -120           -115           -110

gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt      408
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg
          -105           -100           -95

tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac      456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp

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	-90	-85	-80	
ttc atg ttg tat gac gct ctt gat gtt gtt tta tac atg gac cca atg Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met	-75	-70	-65	504
tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu	-60	-55	-50	552
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala	-45	-40	-35	600
tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Asp His Pro	-25	-20	-15	648
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc gct cct act Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr	-10	-5	-1 1	696
gtc aag att gat gct ggg atg gtg gtc ggc acg act act act gtc ccc Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro	5	10	15	744
ggc acc act gcg acc gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala	20	25	30 35	792
tct ccg aca cga ttt gcg cct act cgt ccc gtg cct tgg tca acg Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr	40	45	50	840
cct ttg caa gcc act gca tat ggt cca gca tgc cct caa caa ttc aat Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn	55	60	65	888
tac ccc gaa gaa ctc cgt gag att acg atg gcc tgg ttc aat aca ccg Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro	70	75	80	936
ccc ccg tca gct ggt gaa agt gag gac tgc ctg aac ctc aac atc tac Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr	85	90	95	984
gtc cca gga act gag aac aca aac aaa gcc gtc atg gtt tgg ata tac Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr	100	105	110 115	1032
ggt gga gcg ctg gaa tat ggt tgg aat tca ttc cac ctt tac gac ggg Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly	120	125	130	1080
gct agt ttc gca gcc aat cag gat gtc atc gcc gtg acc atc aac tac Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr	135	140	145	1128

aga acg aac att ctg ggg ttc cct gct gcc cct cag ctt cca ata aca Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr 150 155 160	1176
cag cga aat ctg ggg ttc cta gac caa agg ttt gct ttg gat tgg gta Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val 165 170 175	1224
cag cgg aac atc gca gcc ttt ggc ggt gat cct cga aag gtc aca ata Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile 180 185 190 195	1272
ttt ggg cag agt gcg ggg ggc aga agt gtc gac gtc ctc ttg acg tct Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser 200 205 210	1320
atg cca cac aac cca ccc ttc cga gca gca atc atg gag tcc ggt gtg Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val 215 220 225	1368
gct aac tac aac ttc ccc aag gga gat ttg tcc gaa cct tgg aac acc Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr 230 235 240	1416
act gtt caa gct ctc aac tgt acc acc agt atc gac atc ttg agt tgt Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys 245 250 255	1464
atg aga aga gtc gat ctc gcc act ctg atg aac acg atc gag caa ctc Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu 260 265 270 275	1512
gga ctt ggg ttt gag tac acg ttg gac aac gta acg gct gtg tac cgt Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg 280 285 290	1560
tct gaa acg gct cgc acg act ggt gac att gct cgt gta cct gtt ctc Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu 295 300 305	1608
gtc ggg acg gtg gcc aac gac gga ctt ctc ttt gtc ctc ggg gag aat Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn 310 315 320	1656
gac acc caa gca tat ctc gag gag gca atc ccg aat cag ccc gac ctt Asp Thr Gln Ala Tyr Leu Glu Ala Ile Pro Asn Gln Pro Asp Leu 325 330 335	1704
tac cag act ctc ctt gga gca tat ccc att gga tcc cca ggg atc gga Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly 340 345 350 355	1752
tcg cct caa gat cag att gcc gcc att gag acc gag gta aga ttc cag Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln 360 365 370	1800

tgt cct tct gcc atc gtg gct cag gac tcc cg <sup>g</sup> aat cg <sup>g</sup> ggt atc cct Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro 375 380 385	1848
tct tgg cgc tac tac tac aat g <sup>c</sup> acc ttt gag aat ctg gag ctt ttc Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe 390 395 400	1896
cct ggg tcc gaa gtg tac cac agc tct gaa gtc ggg atg gtg ttt ggc Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly 405 410 415	1944
acg tat cct gtc gca agt g <sup>c</sup> g <sup>c</sup> acc g <sup>c</sup> ttg gag g <sup>c</sup> cag acg agc aaa Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys 420 425 430 435	1992
tac atg cag ggt g <sup>c</sup> tgg g <sup>c</sup> g <sup>c</sup> ttt g <sup>c</sup> aaa aac ccc atg aat g <sup>c</sup> Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly 440 445 450	2040
cct ggg tgg aaa caa gtg cc <sup>g</sup> aat gtc g <sup>c</sup> g <sup>c</sup> ctt g <sup>c</sup> tca cca g <sup>c</sup> Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly 455 460 465	2088
aaa gcc atc cag gtt gac gtc tct cca g <sup>c</sup> aca ata gac caa cga tgt Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys 470 475 480	2136
gcc ttg tac acg cgt tat tat act gag ttg g <sup>c</sup> aca atc g <sup>c</sup> cc <sup>g</sup> agg Ala Leu Tyr Thr Arg Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg 485 490 495	2184
aca ttt g <sup>c</sup> gga g <sup>c</sup> agc g <sup>c</sup> gga g <sup>c</sup> agc g <sup>c</sup> gga g <sup>c</sup> agc aaa gac Thr Phe Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp 500 505 510 515	2232
aac gtt g <sup>c</sup> gac gt <sup>c</sup> gta gt <sup>c</sup> gt <sup>c</sup> g <sup>c</sup> gct g <sup>c</sup> ttg agc ggt ttg gag Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu 520 525 530	2280
acg gca cgc aaa gtc cag g <sup>c</sup> g <sup>c</sup> ggt ctg tcc tgc ctc gtt ctt gag Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu 535 540 545	2328
g <sup>c</sup> atg gat cgt gta g <sup>c</sup> g <sup>c</sup> aag act ctg agc gta caa tcg ggt cc <sup>g</sup> Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro 550 555 560	2376
ggc agg acg act atc aac gac ctc g <sup>c</sup> gct g <sup>c</sup> tgg atc aat gac agc Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser 565 570 575	2424
aac caa agc gaa gta tcc aga ttg ttt gaa aga tt <sup>c</sup> cat ttg gag g <sup>c</sup> Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly 580 585 590 595	2472
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt	2520



820	825	830	835	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat				3240
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp				
840	845	850		
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgga aag				3288
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys				
855	860	865		
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa				3336
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln				
870	875	880		
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc				3384
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala				
885	890	895		
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct				3432
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala				
900	905	910	915	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg				3480
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala				
920	925	930		
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct				3528
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser				
935	940	945		
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga				3576
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg				
950	955	960		
ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag				3618
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala				
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<210> 29

<211> 1205

<212> PRT

<213> Unknown

<220>

<223> gst:esp1:sp:K:trAPAO

<220>

<221> misc\_feature

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<222> (1)..(687)

<223> gst + polylinker

<220>

<221> misc_feature

<222> (2191)..(2226)

<223> spacer sequence

<220>

<221> misc_feature

<222> (2227)..(3615)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (2227)..(2229)

<223> extra lysine

<400> 29

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Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
      -210           -205                   -200

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
      -195           -190                   -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
      -180           -175                   -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
      -165           -160                   -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
      -150           -145                   -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
      -135           -130                   -125

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Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	
-120										-115				-110	
Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg
-105									-100					-95	
Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	Thr	His	Pro	Asp
-90									-85					-80	
Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	Met	Asp	Pro	Met
-75									-70					-65	
Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu
-60									-55					-50	
Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala
-45									-40					-35	
Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro
-25									-20					-15	
Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	Gly	Ser	Pro	Glu	Phe	Ala	Pro	Thr
-10									-5					-1	
Val	Lys	Ile	Asp	Ala	Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro
5									10					15	
Gly	Thr	Thr	Ala	Thr	Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala
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Ser	Pro	Thr	Arg	Phe	Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr
40									45					50	
Pro	Leu	Gln	Ala	Thr	Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn
55									60					65	
Tyr	Pro	Glu	Glu	Leu	Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro
70									75					80	
Pro	Pro	Ser	Ala	Gly	Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr
85									90					95	

Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr  
100 105 110 115

Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly  
120 125 130

Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr  
135 140 145

Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr  
150 155 160

Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val  
165 170 175

Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile  
180 185 190 195

Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser  
200 205 210

Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val  
215 220 225

Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr  
230 235 240

Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys  
245 250 255

Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu  
260 265 270 275

Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg  
280 285 290

Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu  
295 300 305

Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn  
310 315 320

Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu

325	330	335
		Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly
		340 345 350 355
		Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln
	360	365 370
		Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro
	375	380 385
		Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe
	390	395 400
		Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly
	405	410 415
		Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys
	420	425 430 435
		Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly
	440	445 450
		Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly
	455	460 465
		Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys
	470	475 480
		Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg
	485	490 495
		Thr Phe Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp
	500	505 510 515
		Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu
	520	525 530
		Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu
	535	540 545
		Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro
	550	555 560

Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser  
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser  
565 570 575

Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly  
Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly  
580 585 590 595

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly  
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly  
600 605 610

Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val  
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val  
615 620 625

Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu  
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu  
630 635 640

Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu  
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu  
645 650 655

Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro  
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro  
660 665 670 675

Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val  
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val  
680 685 690

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser  
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser  
695 700 705

Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln  
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln  
710 715 720

Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser  
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser  
725 730 735

Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu  
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu  
740 745 750 755

Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala  
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala  
760 765 770

Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr  
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr  
775 780 785

Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu  
790 795 800

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp  
805 810 815

Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser  
820 825 830 835

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp  
840 845 850

Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys  
855 860 865

Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln  
870 875 880

Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala  
885 890 895

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala  
900 905 910 915

Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala  
920 925 930

Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser  
935 940 945

Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
950 955 960

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965 970 975

<210> 30

<211> 3591

<212> DNA

<213> Unknown

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      on vector pGEX-4T-1

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<221> misc_feature

<222> (1)..(687)

<223> gst + polylinker


<220>

<221> mat_peptide

<222> (688)..()

<223> BEST1 mature


<220>

<221> misc_feature

<222> (2164)..(2199)

<223> spacer sequence


<220>

<221> misc_feature

<222> (2200)..(3588)

<223> K:trAPAO


<220>

<221> CDS

<222> (1)..(3588)

<223>
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<220>

<221> misc\_feature

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<223> extra lysine

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Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu		
-210	-205	-200
cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag	135	
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys		
-195	-190	-185
ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat	180	
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp		
-180	-175	-170
ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata	225	
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile		
-165	-160	-155
gct gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca	270	
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala		
-150	-145	-140
gag att tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt	315	
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly		
-135	-130	-125
gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt	360	
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val		
-120	-115	-110
gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt	408	
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg		
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Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp		
-90	-85	-80
ttc atg ttg tat gac gct ctt gat gtt tta tac atg gac cca atg	504	
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met		
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tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa	552	
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu		

-60	-55	-50	
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala			600
-45	-40	-35	-30
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-25	-20	-15	
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc acg gat ttt Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe			696
-10	-5	-1 1	
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85	90	95	
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120	125	130	
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135	140	145	
cgc gag agc ccc acc gga act tcg ggc aac tac ggc cta ctc gac att Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile			1176
150	155	160	
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165	170	175	

gac ccc ggc cga gtg acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala 180 185 190 195	1272
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gct atc ctc gaa aat cca ggg ctg acg cga ccg ctc gcg acg ctc gcc Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala 215 220 225	1368
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cgc tcg acc gac cca gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg 245 250 255	1464
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cgc gcc ttc ctc ggg cgc gcg ccg atg gag acg cca gcg gac tac caa Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln 310 315 320	1656
gcc tat ctg gag gcg cag ttt ggc gac caa gcc gcc gtg gcg gcg Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Val Ala Ala 325 330 335	1704
tgc tat ccc ctc gac ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg 340 345 350 355	1752
atc ttc ggc gac aat cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu 360 365 370	1800
gcg ctt gtg cgc cag ggc gcg ccc gtg tgg cgt tat cag ttc aac qgt Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly 375 380 385	1848
aat acc gag ggt gga aga gcg ccg gct acc cac gga gcc gaa att ccc Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro 390 395 400	1896

tac gtt ttc ggg gtg ttc aag ctc gac gag ttg ggt ctg ttc gat tgg Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp 405 410 415	1944
ccg ccc gag ggg ccc acg ccc gcc gac cgt gcg ctg ggc caa ctg atg Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met 420 425 430 435	1992
tcc tcc gcc tgg gtc cgg ttc gcc aag aat ggc gac ccc gcc ggg gac Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp 440 445 450	2040
gcc ctt acc tgg cct gcc tat tct acg ggc aag tcg acc atg aca ttc Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe 455 460 465	2088
ggt ccc gag ggc cgc gcg gtg gtg tcg ccc gga cct tcc atc ccc Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro 470 475 480	2136
cct tgc gcg gat ggc gcc aag gcg ggg ggc gga ggc agc ggc gga ggc Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Ser Gly Gly Gly 485 490 495	2184
agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly 500 505 510 515	2232
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 520 525 530	2280
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 535 540 545	2328
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 550 555 560	2376
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 565 570 575	2424
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 580 585 590 595	2472
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 600 605 610	2520
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 615 620 625	2568
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	2616

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala			
630	635	640	
agc cct cag gcg aag cg <sup>g</sup> ctc gac agt gtg agc ttc g <sup>c</sup> g <sup>c</sup> cac tac tgt			2664
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys			
645	650	655	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc			2712
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile			
660	665	670	675
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt			2760
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe			
680	685	690	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg			2808
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser			
695	700	705	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag			2856
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln			
710	715	720	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac			2904
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His			
725	730	735	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca			2952
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr			
740	745	750	755
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt			3000
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val			
760	765	770	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt			3048
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu			
775	780	785	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat			3096
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
790	795	800	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc			3144
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
805	810	815	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga			3192
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg			
820	825	830	835
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg			3240
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met			
840	845	850	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga			3288
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg			

855	860	865	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly 870	875	880	3336
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys 885	890	895	3384
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp 900	905	910	3432
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His 920	925	930	3480
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly 935	940	945	3528
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu 950	955	960	3576
gtg cca gca gca tag Val Pro Ala Ala 965			3591

<210> 31

<211> 1196

<212> PRT

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1

<220>

<221> misc\_feature

<222> (1)..(687)

<223> gst + polylinker

<220>

<221> misc\_feature

<222> (2164)..(2199)  
 <223> spacer sequence  
 <220>  
 <221> misc\_feature  
 <222> (2200)..(3588)  
 <223> K:trAPAO  
 <220>  
 <221> misc\_feature  
 <222> (2200)..(2202)  
 <223> extra lysine  
 <400> 31

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	-225	-220	-215	
Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	-210	-205	-200	
His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	-195	-190	-185	
Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	-180	-175	-170	
Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	-165	-160	-155	
Ala	Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	-150	-145	-140	
Glu	Ile	Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	-135	-130	-125	
Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	-120	-115	-110	
Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	-105	-100	-95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp  
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met  
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu  
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala  
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro  
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe  
-10 -5 -1 1

Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp  
5 10 15

Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly  
20 25 30 35

Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg  
40 45 50

Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg  
55 60 65

Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn  
70 75 80

Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val  
85 90 95

Trp Val Tyr Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr  
100 105 110 115

Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe  
120 125 130

Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser  
135 140 145

Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile  
150 155 160

Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly  
165 170 175

Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala  
180 185 190 195

Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly  
200 205 210

Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala  
215 220 225

Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu  
230 235 240

Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg  
245 250 255

Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val  
260 265 270 275

Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly  
280 285 290

Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly  
295 300 305

Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln  
310 315 320

Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala  
325 330 335

Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg  
340 345 350 355

Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu  
360   365   370

Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly  
375   380   385

Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro  
390   395   400

Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp  
405   410   415

Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met  
420   425   430   435

Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp  
440   445   450

Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe  
455   460   465

Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro  
470   475   480

Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly  
485   490   495

Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly  
500   505   510   515

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
520   525   530

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
535   540   545

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
550   555   560

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
565   570   575

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser

580                    585                    590                    595  
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp  
600                    605                    610  
  
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
615                    620                    625  
  
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
630                    635                    640  
  
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
645                    650                    655  
  
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
660                    665                    675  
  
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
680                    685                    690  
  
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
695                    700                    705  
  
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
710                    715                    720  
  
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
725                    730                    735  
  
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
740                    745                    755  
  
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
760                    765                    770  
  
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
775                    780                    785  
  
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
790                    795                    800  
  
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
805                    810                    815

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
820 825 830 835

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
840 845 850

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
855 860 865

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
870 875 880

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
885 890 895

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
900 905 910 915

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
920 925 930

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
935 940 945

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
950 955 960

Val Pro Ala Ala  
965

<210> 32

<211> 1803

<212> DNA

<213> Unknown

<220>

<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<220>

<221> CDS

<222> (1)..(1803)

<223>

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro		
1	5	10
		15
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg		96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Arg Tyr Val		
20	25	30
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct		144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro		
35	40	45
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc		192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys		
50	55	60
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac		240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr		
65	70	75
		80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg		288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly		
85	90	95
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg		336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val		
100	105	110
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc		384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala		
115	120	125
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg		432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc		480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
		160
cag gcc gcc ggt ctg tcc ctc gtt ctt gag ggc acg atg gat cgt gta		528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
165	170	175
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc		576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		

180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val 195	200	205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210	215	220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225	230	235	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245	250	255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260	265	270	816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275	280	285	864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290	295	300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305	310	315	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325	330	335	1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340	345	350	1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355	360	365	1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370	375	380	1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385	390	395	1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405	410	415	1248

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430	1296
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445	1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 595 600	1803

<210> 33

<211> 600

<212> PRT

<213> Unknown

<220>

<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<400> 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
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Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
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Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 34

<211> 37

<212> DNA

<213> Artificial Sequence

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<210> 35		
<211> 1929		
<212> DNA		
<213> Exophiala spinifera		
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<221> Intron		
<222> (739)..(811)		
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<221> Intron		
<222> (1134)..(1186)		
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gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat		180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac		240
tacatcgctcg actacgcccc gagcaaactc accgcaattg gagatgggct gaagtctacc		300
tttgccttg acaggctccc tccttgacag ctggtgccag taccggcctt ggcttcacct		360
gaataacctct ttgagggttga tgccacggcg ctggtgccag gacactcgac cccagacaac		420
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caggccgccc gtctgtcctg cctcggtt gaggcgatgg atcgtgttgg gggaaagact		540

ctgagcgtac	aatcggtcc	cggcaggacg	actatcaacg	acctcggcgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtatccaga	ttgttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	actccccgt	aagcacaatc	ccactttgtg	atgagacctc	tgtcgagtgt	780
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gctccgagcg	ccgtctatgg	gctgaacgat	ctcatcacac	tgggttcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttggaaacg	gagacgtctt	tagttggaa	agggtatatg	1860
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gcagcatag						1929

<210> 36

<211> 600

<212> PRT

<213> Exophilia spinifera

<400> 36

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu  
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp

435

440

445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 37

<211> 1929

<212> DNA

<213> Exophiala spinifera

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

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gacgcggcgttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attgc当地	180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac	240
tacatcgctcg actacgcccc gagcaaactc accgcaattt gagatgggct gaagtctacc	300
tttgc当地tttgc acaggctccc tccttgcacg ctgggtccag taccggcctt ggcttc当地	360
gaataccctct ttgagggttga cgccacggcg ctgggtccag gacactcgac cccagacaac	420
gttgc当地ggacg tggtagtggt gggcgctggc ttgagcggct tggagacggc acgcaaagtc	480
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ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgc当地ggatc	600
aatgacagca accaaagcga agtattccaga ttgtttgaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct	720
ccttatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtg	780
agaatacagt cactgactcc acttcgtcca gctgagcggag gaggttgc当地a gtgc当地ttgc	840
agaatacagt cactgactcc acttcgtcca gctgagcggag gaggttgc当地a gtgc当地ttgc	840
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gagccctc当地g gcgaaggcggc tc当地gactgtg gagttc当地g cactactgtg agaaggacct	960
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cggtgtc当地tc tc当地ggtaggg gactcggttc tt当地gtggc当地a ttccaggtat gc当地gtc当地gatt	1200

tgccatCCA	tgtcaaAGGA	acttGTTCCA	ggctcAGTGC	acctcaACAC	ccccGTCGCT	1260
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cctcttCCCG	ccgagaAGCA	agcattGGCG	gaaaaatCTA	tcctcGGCTA	ctatAGCAAG	1440
atagtCTTCG	tatGGGACAA	cccgtGGTGG	cgcgaACAAAG	gcttctCGGG	cgtCCTCCAA	1500
tcgagCTGTG	accccatCTC	atttGCCAGA	gataCCAGCA	tcgaAGTCGA	tcggCAATGG	1560
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gtacgacAAA	agtctGTCTG	ggaccaACTC	cgcgcAGCCT	acgagaACGC	cggggCCCAA	1680
gtcccAGAGC	cggccaACGT	gctcgaaATC	gagtGGTCGA	agcagcAGTA	tttCCAAGGA	1740
gctccGAGCG	ccgtctATGG	gotgaacGAT	ctcatCACAC	tggGTTcGGC	gctcagaACG	1800
ccgttcaAGT	gtgttcATT	cgttGGAACG	gagacGtCTT	tagttggAA	agggtatATG	1860
gaaggggCCA	tacgatCGGG	tcaacGAGGT	gctgcagaAG	ttgtggCTAG	cctggtgCCA	1920
gcagcatAG						1929

<210> 38

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 38

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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
									20			25			30

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
									35			40			45

Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
									50			55			60

Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
									65			70			80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu  
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 39

<211> 1930

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1187)

<223>

<220>

<221> misc\_feature

<222> (649)..(649)

<223> n = A,T,C or G

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ggaactcctc	cccgatgggt	ctcagctgat	cgaagagcat	agccttcaag	acctcaaggc	900
gagccctcag	gcgaaggccgc	tcgacagtgt	gagctcgcg	cactactgtg	agaaggaact	960
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taatattttc	tcggacaaga	aagacggcg	gcagtatatg	cgatgcacaa	caggtgcgtg	1140
tgggtcgtc	tcaggtgggg	gactcgtttc	tcaagtggtc	atttcaggtt	tgcagtcgtat	1200
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aagcaaaaaag	gtgggtgttt	cgttaccgac	aaccttgtat	cccaccttga	cattttcacc	1380
acctctcccc	gccgagaagc	aagcattggc	ggaaaattct	atcctggct	actatagcaa	1440
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atcgagctgt	gacccatct	catttgccag	agataccagc	atcgacgtcg	atcgacaatg	1560
gtccattacc	tgtttcatgg	tcggagaccc	gggacggaag	tggtcccaac	agtccaagca	1620

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gccgttcaag agtgttcatt tcgttggAAC ggagacgtct ttagttggAA aagggtatat 1860  
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<210> 40

<211> 598

<212> PRT

<213> Exophiala spinifera

<220>

<221> MISC\_FEATURE

<222> (216)..(216)

<223> Xaa = any amino acid

<400> 40

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

85

90

95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
195 200 205

Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr  
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
245 250 255

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
260 265 270

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
275 280 285

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn  
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
325 330 335

Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
340 345 350

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val  
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro  
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly  
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu  
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
450 455 460

Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys  
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
485 490 495

Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn  
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu  
530 535 540

Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser  
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
580 585 590

Ser Leu Val Pro Ala Ala  
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<210> 41

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1185)

<223>

<400> 41

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cacgtcggcg taggccaaa cggaggagg tatgcgacaa tagctggaca gattggacaa 120

gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac 180

ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240

tacatcgctcg actacaaccc gagcaaactc accgcaattg gagatggct gaaggctacc 300

tttgccttg acaggctccc tcctgcacg ctgggccag tgccggccct ggcttcacct	360
gaataccctt ttgagggtga tgccacggcg ctggttccag gacactcaac cccagacaat	420
gttgcggacg tggcgttgtt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc	480
caggctgccc ggctgtcctg cctcggtttt gaggcgatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcggtcc cgccaggacg gctatcaatg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtattcaaa ttatttggaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct	720
ccttatggtg attcccttgtt aagcacaattt ccatttttgtt atgagacctc tgcgtgtgt	780
agaatacagt cgctgactcc acatcggtcca gctgagcgag gaggttgcaa gtgcactcgc	840
ggaactcctt cccgcatggt ctcagctgtt cgaagagcat agtcttgaag accccaaggc	900
gagccctcaa gcgaaggcgc tcgacagtgtt gagcttcgca cactactgtt agaaggatct	960
aagcttgctt gctgttctcg gctgtggcaaa ccagatcaca cgcgtctgc tcgggtgttga	1020
agccccacgag atcagoatgc ttttctcac cgactacatc aagagtgcac ccggctcag	1080
taatattgtc tcggataaga aagacgggtgg gcagttatgtt cgatgcacaaa caggtgcgtt	1140
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gccatgccat gtcaaaggaa ctgtttccag gctcagtgca cctcaacacc cccgtcgccg	1260
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gtaaaaaggt ggtggtttcg ttaccgacaa cttgttatcc caccttgata ttttaccac	1380
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ccattacctt tttcatggtc ggagacccgg gacggaaatgtt gtccttacac tccaaacgg	1620
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tcccagagcc ggccaacgtt ctgcagatcg agtgggtcgaa gcagcgttat ttccaaaggag	1740
cggcgagcgt cgtctatggg ctgaactgtc tcaacacactt ggttccggc ctcagaacgc	1800
cgttcaagggt tggttcatcc gttggaaacgg agacgtttt ggtttggaaa gggtatatgg	1860
aaggggccat acgatcggtt cagcgaggcg ctgcagaatgtt gtcgttagc ctgggtccag	1920
cagcatag	1928

<210> 42

<211> 598

<212> PRT

<213> Rhinocladiella atrovirens

<400> 42

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr  
225 230 235 240

Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu  
245 250 255

Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro  
260 265 270

Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His  
275 280 285

Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn  
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
325 330 335

Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
340 345 350

Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val  
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

405

410

415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly  
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu  
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
450 455 460

Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys  
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
485 490 495

Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn  
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu  
530 535 540

Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly  
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
580 585 590

Ser Leu Val Pro Ala Ala  
595

<210> 43

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

<400> 43  
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gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaga attcgccaac 180  
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
tacatcgctcg actacaaccc gagcaaactc accgcaattg gagatggct gaaggctacc 300  
tttgccttg acaggctccc tccttgacag ctggtgccag tgccggccct ggcttcacct 360  
gaataacctct ttgaggttga tgccacggcg ctggttccag gacactcaac cccagacaat 420  
gttgcggacg tggcgtggg gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480  
caggctgccc ggctgtcctg cctcggttt gaggcgatgg atcgtgtggg gggaaagact 540  
ctgagcgtac aatcggtcc cggcaggacg actatcaatg acctcgccgc tgcgtggatc 600  
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660  
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720  
ccttatggtg attccctgggt aagcacaatt ccatttgtg atgagaccc tcgtgtgtgt 780  
agaatacagt cgctgactcc acatcggtcc gctgagcgag gaggttgcaa gtgcactcgc 840  
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900  
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960

aaacttgcct	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agccccacgag	atcagcatgt	tttttctcac	cgactacatc	aagagtgccca	ccggctctcag	1080
taatattgtc	tcggataaga	aagacggtg	gcagtatatg	cgtgcgtaaa	cagggtgcgtg	1140
tggtgttctc	tca	actcggttct	tagtggtcat	tccaggtatg	cagtcgtt	1200
gccatgccat	gtcaaaggaa	cttggccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgatcc	caccttgata	ttttcaccac	1380
ctcttcccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtgggtgc	gcgaacaagg	cttctcggtc	gtcctccaat	1500
cagactgtga	ccccatctca	tttgcagag	ataccagcat	cgaagtcgt	cggaatgg	1560
ccattacctg	tttcatggtc	ggagacccgg	gacggaagtg	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcbcagccta	cgagaacgcc	ggggcccaag	1680
tcccaagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cggccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcatttc	gttggAACGG	agacgtctt	gtttggaaa	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctgggtccag	1920
cagcatag						1928

<210> 44

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 44

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	Tyr	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val
							20					25			30

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
								35				40			45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys  
195 200 205

Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr  
225 230 235 240

Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu  
245 250 255

Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala  
260 265 270

Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
275 280 285

Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg  
290 295 300

Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr  
305 310 315 320

Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys  
325 330 335

Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu  
340 345 350

Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn  
355 360 365

Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg  
370 375 380

Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr  
385 390 395 400

Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
405 410 415

Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
420 425 430

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
435 440 445

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu  
450 455 460

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
465 470 475 480

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
485 490 495

Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
500 505 510

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
515 520 525

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
580 585 590

<210> 45

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1185)

<223>

<400> 45  
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gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgccaagc attgc当地	180
ctgcgagctt gtcttgctgc agttggagcc acttcaaaccg acattaccaa gctcaattac	240
tacatcgtcg actacaaccc gagcaaactc accgcaattt gagatgggct gaaggctacc	300
tttgc当地tgc acaggctccc tccttgcacg ctgggtccag tgccggccct ggcttc当地ct	360
gaataccctct ttgagggttga tgctacggcg ctgggtccag gacactcaac cccagacaat	420
gttgccggacg tggcgtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc	480
caggctgccc ggctgtccctg ctcgttctt gagggatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgc当地ggatc	600
aatgacagca accaaagcga agtattcaaa ttatttggaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtaacaac cactacagct	720
ccttatggtg attccctggt aggccacaatt ccatcttgc atgagacctc tgc当地gtgt	780
agaatacagt cgctgactcc acatcgtcca gctgagcggag gaggttgcaa gtgc当地tc	840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgc当地 accccaaggc	900
gagccctcaa gcgaaggcgc tcgacagtgt gagcttcgca cactactgt agaaggatct	960
aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgc当地ctgc tcgggtgg	1020
agccccacgag atcagcatgc ttttctcac cgactacatc aagagtgc当地 ccggctc当地	1080
taatattgtc tcggataaga aagacggtg gcagtatatg cgatgc当地aa caggtgc当地	1140
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gccatgccat gtc当地aggaa ctgttccag gctcagtgca cctcaacacc cccgtc当地	1260
aaatttagca gtc当地catcc ggctgtacag tacgatcggc ctgggc当地 gc当地tccgaa	1320
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cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtc当地 cggcaatgg	1560
ccattacctg tttcatggtc ggagacccgg gacggaaatg gtc当地caacag tccaaagg	1620
tacgacagaa gtc当地tctgg aaccacactcc ggc当地ggctta cgagaacgcc gggcccaag	1680
tcccaaggcc ggccaaacgtg ctc当地gatcg agtggtc当地a gc当地cgtat ttccaaggag	1740
cggccgagcgc cgtctatggg ctgaactgta tcaacacact gggttccggc ctc当地aacgc	1800

cgttcaaggg tggcatttc gttggAACGG agacgtcttt ggTTTggaaa gggtatATgg 1860  
aaggggccat acgatcggt cagcgaggcg ctgcagaagt tgtgccttagc ctggtgccag 1920  
cagcatag 1928

<210> 46

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala  
1 5 10 15

Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr  
20 25 30

Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala  
35 40 45

Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu  
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu  
50 55 60

Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr  
65 70 75 80

Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu  
85 90 95

Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro  
100 105 110

Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr  
115 120 125

Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val  
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

145                    150                    155                    160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
165                    170                    175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
180                    185                    190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe  
195                    200                    205

Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
210                    215                    220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
225                    230                    235                    240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
245                    250                    255

Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp  
260                    265                    270

Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala  
275                    280                    285

His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
290                    295                    300

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
305                    310                    315                    320

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
325                    330                    335

Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
340                    345                    350

Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
355                    360                    365

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
370                    375                    380

Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys  
385 390 395 400

Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu  
405 410 415

Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser  
420 425 430

Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser  
435 440 445

Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr  
450 455 460

Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp  
465 470 475 480

Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val  
485 490 495

Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro  
500 505 510

Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe  
515 520 525

Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala  
580 585 590

<210> 47

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile

420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 48

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 48

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aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1           5           10          15

```

48

```

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
          20           25           30

```

96

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35                    40                    45

144

```

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
      50           55           60

```

192

gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65				70					75					80	

240

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
                   85                  90                  95

288

```

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100           105           110

```

336

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg  
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

384

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130	135	140

432

```

cgc ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145          150          155          160

```

480

```
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
```

528

165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttc ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180	185	190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195	200	205	624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210	215	220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225	230	235	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245	250	255	768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260	265	270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275	280	285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290	295	300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305	310	315	960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325	330	335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340	345	350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355	360	365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370	375	380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385	390	395	1200

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248  
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296  
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344  
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 49

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
                  325                 330                 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
           340                   345                   350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 370                    375                    380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 50

aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc			816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			864
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc			912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc			960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac			1008
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga			1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg			1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag			1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa			1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			

435

440

445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 51

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 52

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 52  
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Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg			144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
35	40	45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat			192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg			240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
65	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa			288
Glu Gly Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag			336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg			384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc			576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc			624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc			672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cg <sup>g</sup> aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct qca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460	1392

<210> 53

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile

←

180	185	190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly		
195	200	205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala		
210	215	220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val		
225	230	240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser		
245	250	255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr		
260	265	270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln		
275	280	285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
290	295	300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
305	310	320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
325	330	335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
340	345	350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
355	360	365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
370	375	380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
385	390	400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly		
405	410	415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 54

<211> 11

<212> PRT

<213> Exophiala spinifera

<400> 54

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10